



RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 09/995,419

Source: OIP

Date Processed by STIC: 12/5/01

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PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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OIPE

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DATE: 12/05/2001

PATENT APPLICATION: US/09/995,419

TIME: 10:02:21

Input Set : A:\096,004 - SeqList.ST25.txt

Output Set: N:\CRF3\11212001\I995419.raw

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: Geron Corporation
 4 McWhir, Jim
 5 Gold, Joseph D.
 6 Schiff, J. Michael
 8 <120> TITLE OF INVENTION: 096,004 - SeqList
 10 <130> FILE REFERENCE: 096,004 - SeqList
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 13 <141> CURRENT FILING DATE: 2001-11-26
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 16 <151> PRIOR FILING DATE: 2000-11-27
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370	cctcgagccc	aggcctgcaa	gcgcctccag	aagctggaaa	aagcggggaa	gggaccttc	10320
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378	tttacagaaa	catccaagga	cagggtgaa	gtgcctccgg	gcaagggcag	ggcaggcacg	10560
380	agtgatttta	tttagctatt	ttattttatt	tacttacttt	ctgagacaga	gttatgctct	10620

RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/995,419

TIME: 10:02:21

Input Set : A:\096,004 - SeqList.ST25.txt

Output Set: N:\CRF3\11212001\I995419.raw

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/995,419

DATE: 12/05/2001

TIME: 10:02:22

Input Set : A:\096,004 - SeqList.ST25.txt

Output Set: N:\CRF3\11212001\I995419.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:546 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:548 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:548 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:555 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:557 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:557 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:564 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:566 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:566 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:573 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:575 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:575 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1420 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:1422 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1422 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1429 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:1431 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1431 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1438 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:1440 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1440 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1470 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:1472 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1472 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1485 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:1487 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1487 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

<210> 2
<211> 25
<212> DNA
<213> Artificial

requires <220> to <223>, please see
error summary sheet, item ||

<400> 2
cttgctgcag aagtgggtgg aggaa

25

<210> 3
<211> 21
<212> DNA
<213> Artificial

same

<400> 3
ctgcagtgtg ggtttcgggc a

21

<210> 4
<211> 20
<212> DNA
<213> Artificial

same

<400> 4
cggaagagtg tctggagcaa

20

<210> 5
<211> 19
<212> DNA
<213> Artificial

same

<400> 5
ggatgaagcg gagtctgga

19

<210> 14
<211> 23
<212> DNA
<213> Artificial

— same

<400> 14
ggcctgtact acatttgcct gga

23

<210> 15
<211> 26
<212> DNA
<213> Artificial

<400> 15
gaaatagtgt caagtttcca tcacaa

26

<210> 16
<211> 55
<212> DNA
<213> Artificial

<400> 16
cgatgtggct gcggagccac cggcaggtaa tcctgttgat gctgattgtc tcaac

55

<210> 18
<211> 17
<212> PRT
<213> Artificial

<400> 18

Met Trp Leu Arg Ser His Arg Gln Val Ile Leu Leu Met Leu Ile Val
1 5 10 15

Ser

<210> 19
<211> 17
<212> PRT
<213> Artificial

<400> 19

Met Trp Leu Arg Ser His Arg Gln Val Val Leu Ser Met Leu Leu Val
1 5 10 15

Ser

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/995,419

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 ✓ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 ✓ Use of <220> Sequence(s) 2-5, 14-16, 18, 19 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.